

Fig. 1

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu				
1				5					10					15					
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His				
			20					25					30						
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe				
		35					40					45							
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp				
	50					55					60								
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu				
	65				70					75					80				
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp				
				85					90					95					
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu				
		100						105					110						
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala				
		115					120					125							
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val				
	130					135					140								
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala				
	145				150					155					160				
Cys	Arg	Thr	Gly	Asp															
				165															

Fig. 2

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	
1				5					10					15		
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	
			20					25					30			
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	
		35					40					45				
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	
	50					55					60					
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	
65					70					75					80	
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	
				85					90				95			
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	
		100						105					110			
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	
		115						120				125				
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	
	130					135					140					
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	
145				150					155					160		
Cys	Arg	Thr	Gly	Asp	Arg											
				165												

Fig. 3

```

GGAATTCACCACCATGGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCT
1  -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGACACCGAAGAGGACAGGGA
      M G V H E C P A W L W L L L S L -
GCTGTGCTCCTCTGGGCTCCCAGTCTGGGCGCCCCCCCCGAATCGAGGGCCGCGC
61  -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGGGCTTAGCTCCCGGCGCG
      L S L P L G L P V L G A P P R I E G R A -
CCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
GGGTGGTGCGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT
      P P R L I C D S R V L E R Y L L E A K E -
GGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
181 -----+-----+-----+-----+-----+-----+ 240
CCGGCTCTTATAGTGCTGCCGACACGACTTGTGACGTCGAACTTACTCTTATAGTGACA
      A E N I T T G C A E H C S L N E N I T V -
CCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCCGT
241 -----+-----+-----+-----+-----+-----+ 300
GGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGGCA
      P D T K V N F Y A W K R M E V G Q Q A V -
AGAAGTCTGGCAGGGCCTGGCCCTGCTGTGCGAAGCTGTCCTGCGGGGCCAGGCCCTGTT
301 -----+-----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCCGGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGACAA
      E V W Q G L A L L S E A V L R G Q A L L -
GGTCAACTCTTCCCAGCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
361 -----+-----+-----+-----+-----+-----+ 420
CCAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTCGACGTACACCTATTTTCGGCAGTACC
      V N S S Q P W E P L Q L H V D K A V S G -

```

CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCC
 421 -----+-----+-----+-----+-----+-----+ 480
 GGAAGCGTCGGAGTGCTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGGGG
 L R S L T T L L R A L G A Q K E A I S P -

 TCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCCGCAAAC
 481 -----+-----+-----+-----+-----+-----+ 540
 AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTTGA
 P D A A S A A P L R T I T A D T F R K L -

 CTTCCGAGTCTACTCCAATTTCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG
 541 -----+-----+-----+-----+-----+-----+ 600
 GAAGGCTCAGATGAGGTTAAAGGAGGCCCTTCGACTTCGACATGTGTCCCCTCCGGAC
 F R V Y S N F L R G K L K L Y T G E A C -

 CAGGACAGGGGACAGATGACCAGGTCGAC
 601 -----+-----+-----+-----+-----+ 629
 GTCCTGTCCCCTGTCTACTGGTCCAGCTG
 R T G D R * -

Fig. 4

GGAATTCACCACCATGGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCT
1 -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGACACCGAAGAGGACAGGGA
M G V H E C P A W L W L L L S L -
GCTGTGCTCCTCTGGGCTCCAGTCTGGGCGCCCCCGCCCCACACGCCTCAT
61 -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGCGGGGTGGTGGGAGTA
L S L P L G L P V L G A P P A P P R L I -
CTGTGACAGCCGAGTCTGGAGAGGTACCTCTTGAGGCCAAGGAGGCCGAGAATATCAC
121 -----+-----+-----+-----+-----+-----+ 180
GACACTGTGCGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCTCCGGCTCTTATAGTG
C D S R V L E R Y L L E A K E A E N I T -
GACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGTCCCAGACACCAAAGT
181 -----+-----+-----+-----+-----+-----+ 240
CTGCCCGACACGACTTGTGACGTGGAACCTACTCTTATAGTGACAGGGTCTGTGGTTTCA
T G C A E H C S L N E N I T V P D T K V -
TAATTTCTATGCCTGGAAGAGGATGGAGGTGCGGCAGCAGGCCGTAGAAGTCTGGCAGGG
241 -----+-----+-----+-----+-----+-----+ 300
ATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCGGGCATCTTCAGACCGTCCC
N F Y A W K R M E V G Q Q A V E V W Q G -
CCTGGCCCTGCTGTGGAAGCTGTCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCCCA
301 -----+-----+-----+-----+-----+-----+ 360
GGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGACAACCAGTTGAGAAGGGT
L A L L S E A V L R G Q A L L V N S S Q -
GCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGGCCTTCGCAGCCTCAC
361 -----+-----+-----+-----+-----+-----+ 420
CGGCACCCTCGGGGACGTGACGTACACCTATTTCCGGCAGTCACCGGAAGCGTCGGAGTG
P W E P L Q L H V D K A V S G L R S L T -

CACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCCTCCAGATGCGGCCTC
 421 -----+-----+-----+-----+-----+ 480
 GTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGGGGAGGTCTACGCCGGAG
 T L L R A L G A Q K E A I S P P D A A S -

 AGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAACCTCTCCGAGTCTACTC
 481 -----+-----+-----+-----+-----+ 540
 TCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTTGAGAAGGCTCAGATGAG
 A A P L R T I T A D T F R K L F R V Y S -

 CAATTTCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAGGGGACAG
 541 -----+-----+-----+-----+-----+ 600
 GTTAAAGGAGGCCCTTTCGACTTCGACATGTGTCCCCTCCGGACGTCCTGTCCCCTGTC
 N F L R G K L K L Y T G E A C R T G D R -

 ATGACCAGGTCGAC
 601 -----+----- 614
 TACTGGTCCAGCTG
 * -

Fig. 5

```

GGAATTCACCACCATGGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCT
1  -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGACACCGAAGAGGACAGGGA
      M G V H E C P A W L W L L L S L -

GCTGTCGCTCCCTCTGGGCCTCCCAGTCCTGGGCGCCCCCGGCGCCGCCCCTACGC
61  -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGCCGCGGCGGGTGATGCG
      L S L P L G L P V L G A P P G A A H Y A -

CCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGAGGCCAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
GGGTGGTGGCGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT
      P P R L I C D S R V L E R Y L L E A K E -

GGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
181 -----+-----+-----+-----+-----+-----+ 240
CCGGCTCTTATAGTGCTGCCCGACACGACTTGTGACGTGGAACCTACTCTTATAGTGACA
      A E N I T T G C A E H C S L N E N I T V -

CCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCCGT
241 -----+-----+-----+-----+-----+-----+ 300
GGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGGCA
      P D T K V N F Y A W K R M E V G Q Q A V -

AGAAGTCTGGCAGGGCCTGGCCCTGCTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTT
301 -----+-----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCCGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGACAA
      E V W Q G L A L L S E A V L R G Q A L L -

GGTCAACTCTTCCCAGCCGTGGGAGCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
361 -----+-----+-----+-----+-----+-----+ 420
CCAGTTGAGAAGGGTGGGCACCTCGGGGACGTCGACGTACACCTATTTGCGCAGTCACC
      V N S S Q P W E P L Q L H V D K A V S G -

```

CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCC
 421 -----+-----+-----+-----+-----+-----+ 480
 GGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGGGG
 L R S L T T L L R A L G A Q K E A I S P -

 TCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAACT
 481 -----+-----+-----+-----+-----+-----+ 540
 AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTTGA
 P D A A S A A P L R T I T A D T F R K L -

 CTTCCGAGTCTACTCCAATTTCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG
 541 -----+-----+-----+-----+-----+-----+ 600
 GAAGGCTCAGATGAGGTAAAGGAGGCCCTTTTCTGACTTCGACATGTGTCCCCTCCGGAC
 F R V Y S N F L R G K L K L Y T G E A C -

 CAĠGACAGGGGACAGATGACCAGGTCGAC
 601 -----+-----+-----+-----+-----+ 629
 GTCCTGTCCCCTGTCTACTGGTCCAGCTG
 R T G D R * -